

Chapter 17 – GENOMES

Exercises.

1. The gene most responsible for differences in size among different breeds of dogs is the _____ gene.
- a. myostatin
 - b. phosphofructokinase
 - c. insulin-like growth factor
 - d. tyrosine growth factor
 - e. giant

Answer: C

2. Dideoxynucleoside triphosphates (ddNTPs) are used to
- a. synthesize DNA strands.
 - b. serve as primers.
 - c. stop the replication of a DNA strand.
 - d. amplify DNA fragments.

Answer: c

- 3*. Suppose a long sequence of DNA is cut with four different restriction enzymes. Which restriction enzyme should produce the fewest number of fragments?
- a. One that cuts at the sequence GACT
 - b. One that cuts at the sequence GCCTCT
 - c. One that cuts at the sequence AGTTCTAT
 - d. One that cuts at the sequence CAGTTCTATG
 - e. Each of these enzymes should produce roughly the same number of fragments.

Answer: d

- 4*. A DNA sequence is cut by two different restriction enzymes (A and B). Digestion from enzyme A yields the following fragments (read 5' to 3'): CGATAC, GTCGTCGCC, GTTATCGCGAC. Digestion from enzyme B yields the following fragments (read 5' to 3'): CGACGTCGTCGCC, CGATACGTTATCG. What was the original sequence?
- a. CGACGTCGTCGCCCGATACGTTATCG
 - b. GTCGTCGCCCGATACGTTATCGCGAC
 - c. CGATACGTTATCGCGACGTCGTCGCC
 - d. CGATACGTCGTCGCCGTTATCGCGAC
 - e. None of the above

Answer: C

5. What is the major disadvantage of hierarchical sequencing as compared to shotgun sequencing?

- a. Hierarchical sequencing requires more sophisticated computer algorithms.
- b. Hierarchical sequencing requires special restriction enzymes, whereas shotgun sequencing does not.
- c. Hierarchical sequencing requires more steps than shotgun sequencing, and hence is slower.
- d. Both a and b are disadvantages.
- e. None of the above is a disadvantage.

Answer: C

6. In what way does a ddNTP differ from its dNTP counterparts?

- a. The ddNTP has an extra —COOH group.
- b. The ddNTP has an extra —OH group.
- c. The ddNTP is missing an —OH group.
- d. The ddNTP is a doublet of the dNTP.
- e. The ddNTP is not attached to the base.

Answer: C

7*. In DNA sequencing, ddNTPs are added at much lower concentrations than are dNTPs. If ddNTPs were added at higher concentrations, what would be the most likely result?

- a. The ddNTPs would bind to one another.
- b. All of the reactions would terminate early and long strands would not be produced.
- c. The reactions would terminate early or late.
- d. The ddNTPs would bind to DNA polymerase.
- e. The ddNTPs would not bind to the dye.

Answer: b

8. Which of the following would *not* be required for the purpose of determining the sequence of a 400-base-pair DNA fragment by the standard ddNTP sequencing method?

- a. The four dNTPs (dATP, dCTP, dGTP, dTTP)
- b. DNA polymerase
- c. A short, artificially synthesized primer
- d. A bacterial artificial chromosome
- e. All of the above would be required.

Answer: d

9. A promoter is an example of a(n)

- a. open reading frame.
- b. transposable element.
- c. chromatin sequence.

- d. rRNA gene.
- e. regulatory sequence.

Answer: e

10. Which of the following statements about chromosome structure and function is *false*?

- a. Telomere sequences are found at the ends of chromosomes.
- b. Remodeling of chromatin structure can alter gene expression.
- c. A chromosome has a single DNA molecule.
- d. Short tandem repeats are an example of noncoding DNA.
- e. All of the above are true; none is false.

Answer: e

11*. A lab sequencing the DNA of various species of pathogenic bacteria with the goal of determining their evolutionary relationships would be practicing _____ genomics.

- a. functional
- b. operational
- c. meta-
- d. comparative
- e. eukaryotic

Answer: d

12. The first free-living organism to have its complete genome sequenced was

- a. the bacterium *Haemophilus influenzae*.
- b. the bacterium *Mycoplasma genitalium*.
- c. the fruit fly *Drosophila melanogaster*.
- d. the typhus-causing bacterium *Rickettsia prowazekii*.
- e. *E. coli* strain 0157:H7.

Answer: a

13*. Craig Venter, a leader of one of the teams that sequenced the human genome, has now turned his attention to cataloging the microbial life of the oceans. His studies, which involve PCR amplification of microbial DNA and a sequencing of the PCR products, are part of a field of biology called

- a. functional genomics.
- b. transposon-tagging.
- c. proteomics.
- d. phenomics.
- e. metagenomics.

Answer: e

14. Which of the following is *least* likely to be associated with metagenomics?

- a. Bacterial culture techniques

- b. Shotgun sequencing
- c. Comparative genomics
- d. PCR
- e. Sampling from the field

Answer: a

15. Which of the following is likely to be found in a eukaryotic genome but *not* in a prokaryotic one?

- a. Regulatory sequences
- b. Coding sequences
- c. Open reading frames
- d. RNA genes
- e. Telomeric sequences

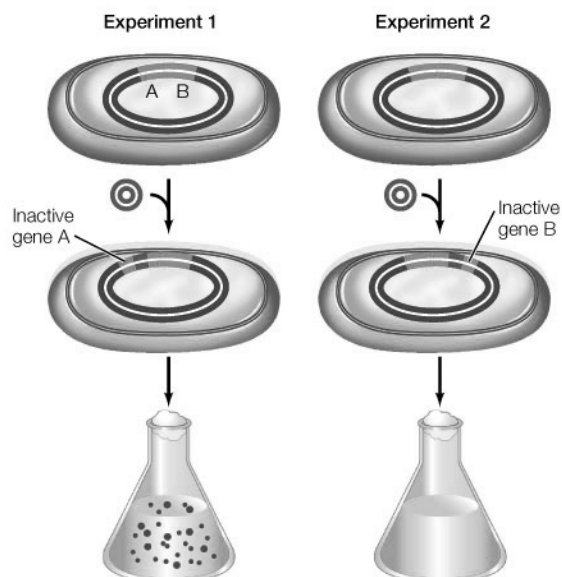
Answer: e

16. Which of the following statements about genomes is true?

- a. Most genes found in the genomes of complex multicellular organisms are not required for survival.
- b. As complexity increases from bacteria to yeast to invertebrate to vertebrate, gene number increases more than does the size of the genome.
- c. As complexity increases from bacteria to yeast to invertebrate to vertebrate, the proportion of the genome consisting of coding sequence increases.
- d. Both a and b
- e. Both b and c

Answer: a

17*. The diagram below shows the use of transposons as mutagens.



17.1. Based on the diagram, which of the following is true?

- a. Gene A is essential because there was growth when gene A was mutagenized.
- b. Gene A is not essential because there was growth when gene A was mutagenized.
- c. Gene A is not essential because there was no growth when gene A was mutagenized.
- d. Gene A is essential because there was no growth when gene A was mutagenized.
- e. Whether gene A is essential or not depends on gene B.

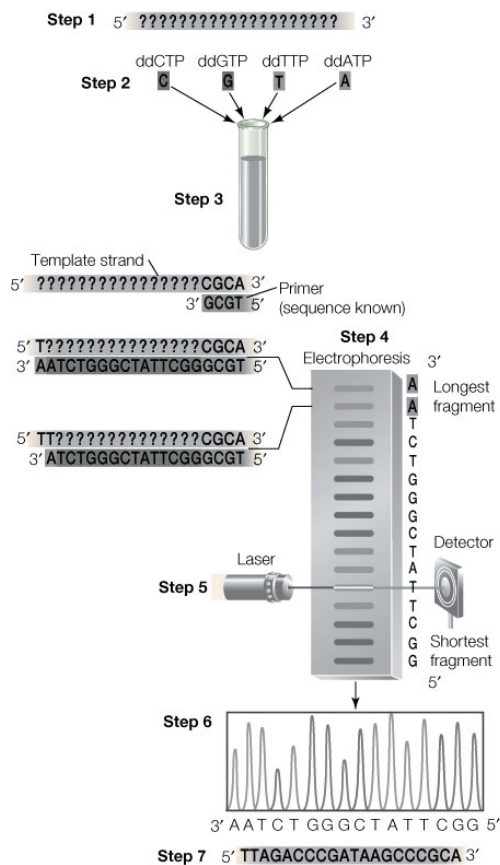
Answer: b

17.2. Studies like those shown in the diagram would be most useful for questions related to

- a. the metabolome.
- b. proteomics.
- c. metagenomics.
- d. bacterial artificial chromosomes.
- e. determining minimal genome size.

Answer: c

18*. The diagram below shows how DNA is sequenced.



18.1. At which step can DNA synthesis be halted by the incorporation of a ddNTP?

- a. Step 2
- b. Step 3
- c. Step 4
- d. Step 5
- e. Step 6 or later

Answer: b

18.2. At which step are the DNA segments first separated by length?

- a. Step 2
- b. Step 3
- c. Step 4
- d. Step 5
- e. Step 6 or later

Answer: C

19. What is the most likely explanation for the abundance of transposons in eukaryotic genomes?

- a. They are needed to provide mutations.
- b. They are needed to increase genetic recombination.
- c. They are genomic parasites.
- d. They assist in the process of DNA repair.
- e. They provide reverse transcriptase.

Answer: C

20. Which of the following statements comparing the human genome to that of invertebrates like *C. elegans* and *D. melanogaster* is true?

- a. A larger fraction of DNA in the human genome is for coding proteins.
- b. The human genome is more than ten times larger.
- c. The average human gene codes for more proteins than the average invertebrate gene.
- d. Both a and b
- e. Both b and c

Answer: C

21*. Genomics has revealed that the bacterium that causes tuberculosis has more 250 genes that metabolize lipids. What does this finding suggest about the bacterium and about medicinal approaches to this disease?

Answer: **The tuberculosis bacterium must use lipids as a source of energy-rich compounds; inhibiting lipid synthesis**

22*. Analyzing the human genome has revealed many genes that cause disease when mutated. Why have we not been able to eliminate those diseases now that we know the genes that are involved?

Answer: **We have not been able to eliminate genetic diseases because, except in a few rare cases, we are not able to replace the mutated genes in the diseased individual. If those genes play a role in development, they need to be identified and replaced in the early embryo.**